wherein said PEG-3 promoter has PEG-3 promoter activity and is about 464 nucleotides long, the entire length of which is at least about 95% identical to the sequence of nucleotides 1507 to 1970 of SEQ ID NO:1.

B4 cont'd

[Please **add** new claim 40 as follows:]

40. (NEW) The isolated nucleic acid of claim 39, wherein the entire length of the PEG-3 promoter is at least about 99% identical to the sequence of nucleotides 1507 to 1970 of SEQ ID NO:1.

IN THE SPECIFICATION

Please **insert** the following paragraph at page 1, line 6, before the first paragraph of the application:

B5

This application is a continuation-in-part application of U.S. Patent Application No. 09/052,753, filed March 31, 1998, which is a continuation-in-part application of International Application No. PCT/US98/05793, filed March 20, 1998.

Please **delete** the Sequence Listing of record and **substitute**, therefor, the Substitute Sequence Listing attached hereto.

Please **amend** the paragraph beginning at page 2, line 3 and ending at page 2, line 26 with the following rewritten paragraph:

This invention provides for an isolated nucleic acid comprising a PEG-3 promoter comprising the nucleotide sequence beginning with the guanosine (G) at position -270 and ending with the cytosine (C) at position +194 of Figure 2 (nucleotides 1507-1970 of SEQ ID NO:1). The invention also provides for a method for identifying an agent which modulates PEG-3 promoter activity in a cell which comprises: (a) contacting the cell with the agent wherein the cell comprises a nucleic acid comprising a PEG-3 promoter operatively linked to a reporter gene; (b) measuring the level of reporter gene expression in the cell; and (c) comparing the expression level measured in step (b) with the reporter gene expression level measured in an identical cell in the absence of the agent, wherein a lower expression level measured in the presence of the agent is indicative of an agent that inhibits PEG-3 promoter activity and wherein a higher expression level measured in the presence of the agent is indicative of an

agent that enhances PEG-3 promoter activity, thereby identifying an agent which modulates PEG-3 promoter activity in the cell. The invention provides a method for treating cancer in a subject which comprises administering a nucleic acid comprising a PEG-3 promoter operatively linked to a gene-of-interest wherein the gene of interest is selectively expressed in cancerous cells in the subject and such expression results in growth suppression or death of the cancerous cells, thereby treating cancer in the subject.

Please **amend** the paragraph beginning at page 7, line 14 and ending at page 7, line 17 with the following rewritten paragraph:

This invention provides for an isolated nucleic acid comprising a PEG-3 promoter comprising the nucleotide sequence beginning with the guanosine (G) at position -270 and ending with the cytosine (C) at position +194 of Figure 2 (nucleotides 1507-1970 of SEQ ID NO:1).

Please **amend** the paragraph beginning at page 7, line 19 and ending at page 7, line 21 with the following rewritten paragraph:

B9

The invention also provides an isolated nucleic acid comprising a fragment of the nucleotide sequence of nucleotides -270 to +194 of Figure 2 (residues 1507-1970 of SEQ ID NO:1) which is at least 15 nucleotides in length.

Please **amend** the paragraph beginning at page 7, line 25 and ending at page 7, line 28 with the following rewritten paragraph:

B10

(i) a PEA3 protein binding sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position -105 and ending with the thymidine (T) at position -100 of Figure 2 (nucleotides 1672-1677 of SEQ ID NO:1),

Please **amend** the paragraph beginning at page 7, line 30 and ending at page 7, line 32 with the following rewritten paragraph:

B11

(ii) a TATA sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position -29 and ending with the adenosine (A) at

B11 cancel

position -24 of Figure 2 (nucleotides 1748-1753 of SEQ ID NO:1), or

Please **amend** the paragraph beginning at page 8, line 1 and ending at page 8, line 4 with the following rewritten paragraph:

B12

(iii) an AP1 protein binding sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position +5 and ending with the adenosine (A) at position +11 of the nucleotide sequence shown in Figure 2 (nucleotides 1781-1787 of SEQ ID NO:1).

Please **amend** the paragraph beginning at page 10, line 13 and ending at page 10, line 19 with the following rewritten paragraph:

B13

The invention provides for a method for treating cancer in a subject which comprises administering a nucleic acid comprising a PEG-3 promoter operatively linked to a gene-of-interest wherein the gene-of-interest is selectively expressed in cancerous cells in the subject and such expression results in growth suppression or death of the cancerous cells, thereby treating cancer in the subject.

Please **amend** the paragraph beginning at page 10, line 21 and ending at page 10, line 31 with the following rewritten paragraph:

B14

In one embodiment of this invention, the nucleic acid consists essentially of (i) a PEA3 protein binding sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position -105 and ending with the thymidine (T) at position -100 of Figure 2, (ii) a TATA sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position -29 and ending with the adenosine (A) at position -24 of Figure 2, and (iii) an AP1 protein binding sequence consisting of the nucleotide sequence beginning with the thymidine (T) at position +5 and ending with the adenosine (A) at position +11 of the nucleotide sequence shown in Figure 2.

Please **amend** the paragraph beginning at page 44, line 20 and ending at page 45, line 22 with the following rewritten paragraph:

B15

To define the region(s) of the FL-PEG-Prom involved in the differential expression of the PEG-3 gene during progression of the transformed phenotype in H5tsl25-transformed cells, a series of PEG-Prom deletion constructs were engineered and placed in front of the luciferase gene

(Fig. 5 and 6). Deletion of the PEA3 site at position -1645 and the TATA box at position -1072 did not effect PEG promoter activity in either E11 or E11-NMT suggesting that these regions of the promoter do not contribute to basal or enhanced expression of the PEG-Prom in E11 or E11-NMT cells (Fig. 5). A further deletion at position -270 minimally inhibited promoter activity in E11-NMT cells (~19% reduction versus activity of the FL-PEG-Prom) without significantly altering activity of the PEG-Prom in E11 cells. In contrast, removal of the PEA3 site at -104 nt with retention of the TATA box at position -24 and the AP1 site at +8 bp resulted in a reduction in basal promoter activity in both E11 and E11-NMT cells. The activity of this mutant PEG-Prom was 15- and 4-fold lower, respectively, than the activity of the FL-PEG-Prom in E11-NMT and E11 cells (Fig. 5). In effect, this promoter deletion eliminated the enhanced expression of the PEG-Prom in E11-NMT versus E11 cells, indicating that the PEA3 site at -104 is a primary determinant of the enhanced activity of PEG-3 in progressed H5ts125-transformed RE cells. Internal deletions at position -1167 to -536 and -1287 to -361 resulted in similar levels of luciferase activity in E11-NMT and E11 cells as observed with the deletion mutant containing a deletion at position -270. Internal deletions

engineered between -1167 to -142 and -1590 to -142 resulted in a further decrease in promoter activity in both E11 and E11-NMT cells, with the most profound effect apparent in E11-NMT cells (~41% reduction in activity in comparison with the FL-PEG-Prom). In contrast, deletion of the promoter regions from -142, -536 or -1167 with retention of the remainder of the PEG-Prom completely abolished PEG promoter activity (Fig. 5). These results implicate the PEA3 transcription site (at position -104), the AP1 transcription site (at position +8) and the TATA box (at position -24) as primary determinants of basal PEG-Prom activity in E11 and E11-NMT cells.

Please **amend** the paragraph beginning at page 56 line 22 and ending at page 57 line 9 as follows:

Nuclear extracts were prepared from 2 to 5 X 10^8 cells as described by Dignam *et al.* (1983). The sequence of probes were as follows: wild-type AP1, 5'CGCAGATTGACTCAGTTCGC3' (SEQ ID NO:5)/ 3''GCGTCTAACTGAGTCAAGCG 5' (SEQ ID NO:6); mutant AP1, 5'CGCAGATAAACTACGTTCGC 3' (SEQ ID NO:7)/ 3' GCGTCTATTTGATGCAAGCG 5' (SEQ ID NO:8); wild-type PEA3, 5' GTGTTGTTTTCCTCTCTCCA 3' (SEQ ID NO:9)/ 3' CACAACAAAAGGAGAGAGGT 5' (SEQ ID NO:10); and mutant PEA3', 5' GTGTTGTTCCCATCTCTCCA 3' (SEQ ID NO:11)/ 3'

CACAACAAGGGTAGAGAGGT 5' (SEQ ID NO:12). The double-stranded oligonucleotides were labeled with ^{32}P-ATP (Amersham) and T4 polynucleotide kinase. The labeled probes were then incubated with nuclear extract at RT for 30 min. The reaction mixture consisted of ^{32}P-labeled deoxynucleotides (>5000 cpm), 2 µg of poly(dI-dC) and 10 µg of nuclear protein extract with 10 mM HEPES (pH 7.5), 50 mM KCI, 5 mM MgCI2, 0.5 mM EDTA, 1 mM DTT and 12.5% glycerol.

After incubation for 30 min at RT, the reaction mixtures were electrophoresed on a 5% polyacrylamide gel with 0.5 X TBE (160V for 3 h). The gel was dried and autoradiographed. Nuclear extracts were also incubated with a 10- or 100-fold molar excess of cold competitor oligonucleotide or cJun (AP1), PEA3 or actin antibody (1 or 5 µtogether with the ^{32}P-labeled probe.

Please **delete** the abstract of record and substitute, therefor, the following rewritten abstract: